

SEQUENCE LISTING

<110> Booth, Russ
 Cahoon, Rebecca E
 Hitz, William D
 Kinney, Anthony
 Yadav, Naren

<120> Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-ACP Desaturase

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Case	Age	Sex	Duration	Location	Findings	Comments
1	25	M	10 years	Left eye	Small, dark, pigmented lesion	Benign melanocytic nevus
2	35	F	5 years	Right eye	Large, raised, pigmented lesion	Malignant melanoma
3	45	M	15 years	Left eye	Small, dark, pigmented lesion	Benign melanocytic nevus
4	55	F	20 years	Right eye	Large, raised, pigmented lesion	Malignant melanoma
5	65	M	25 years	Left eye	Small, dark, pigmented lesion	Benign melanocytic nevus
6	75	F	30 years	Right eye	Large, raised, pigmented lesion	Malignant melanoma
7	85	M	35 years	Left eye	Small, dark, pigmented lesion	Benign melanocytic nevus
8	95	F	40 years	Right eye	Large, raised, pigmented lesion	Malignant melanoma

Met Leu Ser Ile Ile Phe Lys Glu Phe Val Lys Tyr Asn Arg His Val
1 5 10 15

Leu Pro Gln Leu Pro Cys Ser Ser Arg Lys Ala His His Arg His Leu
35 40 45

Lys Ala His Ser Met Pro Pro Glu Lys Lys Glu Ile Phe Lys Ser Leu
65 70 75 80

Gln Cys Trp Gln Pro Gln Asn Phe Leu Pro Asp Pro Ser Leu Pro His
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Leu Pro Asp Glu Tyr Phe Val Val Leu Val Gly Asp Met Val Thr Glu
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Asp Ala Leu Pro Thr Tyr Gln Thr Met Ile Asn Asn Leu Asp Gly Val
145 150 155 160

Lys Asp Asp Ser Gly Thr Ser Pro Ser Pro Trp Ala Val Trp Thr Arg
165 170 175

Ala Trp Thr Ala Glu Glu Asn Arg His Gly Asp Leu Leu Arg Thr Tyr
180 185 190

Leu Tyr Leu Ser Gly Arg Val Asp Met ala Lys Val Glu Lys Thr Val
195 200 205

His Tyr Leu Ile Ser Ala Gly Met Asp Pro Gly Thr Asp Asn Asn Pro
210 215 220

Tyr Leu Gly Phe Val Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Val
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Ala His Gly Asn Thr Ala Arg Leu Ala Lys Glu Gly Gly Asp Pro Val
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Leu Ala Arg Leu Cys Gly Thr Ile Ala Ala Asp Glu Lys Arg His Glu
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Asn Ala Tyr Ser Arg Ile Val Glu Lys Leu Leu Glu Val Asp Pro Thr
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Gly Ala Met Val Ala Ile Gly Asn Met Met Glu Lys Lys Ile Thr Met
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Pro Ala His Leu Met Tyr Asp Gly Asp Asp Pro Arg Leu Phe Glu His
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 Glu Gly Leu Met ala Glu Gly Lys Arg Ala Gln Asp Phe Val Cys Gly
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 35 40 45

 Cys Arg Ser Ser His Ser Ser Thr Gly Thr Thr Thr Met ala Val Pro
 50 55 60

 Val Leu Lys Arg Arg Glu Lys Gln Asp Glu Xaa Gln Glu Trp Met Gly
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 Tyr Leu Ala Pro Glu Lys Leu Glu Val Leu Ala His Leu Glu Pro Trp
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 Ala Glu Ala His Val Leu Pro Leu Leu Lys Pro Ala Glu Glu
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Val Gly Ala Pro Ala Ala Arg Ala Arg Val Thr His Ser Met Pro Pro
      35             40             45

Glu Lys Ala Glu Val Phe Arg Ser Leu Glu Gly Trp Ala Ala Arg Ser
      50             55             60

Leu Leu Pro Leu Leu Lys Pro Val Glu Glu Cys Trp Gln Pro Ala Asp
      65             70             75             80

Phe Leu Pro Asp Ser Ser Ser Glu Met Phe Gly His Glu Val Arg Glu
      85             90             95

Leu Arg Ala Arg Ala Ala Gly Leu Pro Asp Glu Tyr Phe Val Val Leu
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Val Gly Asp Met Val Thr Glu Glu Ala Leu Pro Thr Tyr Gln Thr Met
      115            120            125

Ile Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala Ser Asn Cys
      130            135            140

Pro Trp Ala Val Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn Arg His
      145            150            155            160

Gly Asp Ile Leu Gly Lys Tyr Met Tyr Leu Ser Gly Arg Val Asp Met
      165            170            175

Arg Met Val Glu Lys Thr Val Gln Tyr Leu Ile Gly Ser Gly Met Asp
      180            185            190

Pro Gly Thr Glu Asn Asn Pro Tyr Leu Gly Phe Val Tyr Thr Ser Phe
      195            200            205

Gln Glu Arg Ala Thr Ala Val Ser His Gly Asn Thr Ala Arg Leu Pro
      210            215            220

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Arg Ala His Gly Asp Asp Phe Leu Ala Arg Ala Cys Gly Thr Asn Arg
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Val
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 35 40 45
 His Gly Asn Thr Ala Arg Leu Val Gly Ala Arg Gly His Gly Asp Ala
 50 55 60
 Ala Leu Ala Arg Val Cys Gly Thr Val Ala Ala Asp Glu Lys Arg His
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 Glu Ala Ala Tyr Thr Arg Ile Val Ser Arg Leu Leu Glu Ala Asp Pro
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<400> 10

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Ser	Ser	Ala	Arg	Thr	Arg	Val	Thr	Leu	Pro	Gln	Ile	Ile	His	Trp	Arg	35	40	45	
Cys	Arg	Ser	Ser	His	Ser	Ser	Thr	Gly	Thr	Thr	Thr	Met	Ala	Val	Pro	50	55	60	
Val	Leu	Lys	Arg	Arg	Glu	Lys	Gln	Asp	Glu	Glu	Gln	Glu	Trp	Met	Gly	65	70	75	80
Tyr	Leu	Ala	Pro	Glu	Lys	Leu	Glu	Val	Leu	Ala	His	Leu	Glu	Pro	Trp	85	90	95	
Ala	Glu	Ala	His	Val	Leu	Pro	Leu	Leu	Lys	Pro	Ala	Glu	Glu	Ala	Trp	100	105	110	
Gln	Pro	Ser	Asp	Met	Leu	Pro	Asp	Pro	Ala	Ala	Leu	Gly	Asp	Glu	Gly	115	120	125	
Phe	His	Asp	Ala	Cys	Arg	Glu	Leu	Arg	Ala	Arg	Ala	Ala	Ser	Val	Pro	130	135	140	
Asp	Ala	His	Leu	Val	Cys	Leu	Val	Gly	Asn	Met	Ile	Thr	Glu	Glu	Ala	145	150	155	160
Leu	Pro	Thr	Tyr	Gln	Ser	Val	Pro	Asn	Arg	Phe	Glu	Ala	Val	Arg	Asp	165	170	175	
Leu	Thr	Gly	Ala	Asp	Ser	Thr	Ala	Trp	Ala	Arg	Trp	Ile	Arg	Gly	Trp	180	185	190	
Ser	Ala	Glu	Glu	Asn	Arg	His	Gly	Asp	Ala	Leu	Ser	His	Tyr	Met	Tyr	195	200	205	
Leu	Ser	Gly	Arg	Val	Asp	Met	Arg	Gln	Val	Asp	Arg	Thr	Val	His	Arg	210	215	220	
Leu	Ile	Ala	Ser	Gly	Met	Ala	Met	Asn	Ala	Ala	Arg	Ser	Pro	Tyr	His	225	230	235	240
Gly	Phe	Ile	Tyr	Val	Ala	Phe	Gln	Glu	Arg	Ala	Thr	Ala	Ile	Ser	His	245	250	255	
Gly	Asn	Met	Ala	Arg	His	Val	Gly	Ala	His	Gly	Asp	His	Val	Leu	Ala	260	265	270	

Arg Val Cys Gly Ala Ile Met Ala Asp Glu Lys Arg His Glu Thr Ala
 275 280 285
 Tyr Thr Arg Ile Val Ala Lys Leu Phe Glu Val Asp Pro Asp Ala Ala
 290 295 300
 Val Arg Ala Leu Gly Tyr Met Met Arg His Arg Ile Thr Met Pro Ala
 305 310 315 320
 Ala Leu Met Thr Asp Gly Arg Asp Ala His Leu Tyr Ala His Tyr Ala
 325 330 335
 Ala Ala Ala Gln Gln Thr Gly Val Tyr Thr Ala Ser Asp Tyr Arg Ser
 340 345 350
 Ile Leu Glu His Leu Ile Arg Gln Trp Arg Val Glu Glu Leu Ala Ala
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 Gly Leu Ser Gly Glu Gly Arg Arg Ala Arg Asp Tyr Val Cys Gly Leu
 370 375 380
 Pro His Lys Ile Arg Arg Met Glu Glu Lys Ala His Asp Arg Ala Ala
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Met Arg Lys Arg Ile Thr Met Pro Ala His Leu Met His Asp Gly Arg
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Asp Met Asp Leu Phe Glu His Phe Ala Ala Val Ala Gln Arg Leu Gly
290 295 300

Val Tyr Thr Ala Arg Asp Tyr Ala Asp Ile Val Glu Phe Leu Val Lys
305 310 315 320

Arg Trp Lys Leu Glu Thr Leu Glu Ser Gly Leu Ser Gly Glu Gly Arg
325 330 335

Arg Ala Arg Asp Phe Val Cys Gly Leu Ala Pro Arg Met Arg Arg Ala
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Ala Glu Arg Ala Glu Asp Arg Ala Lys Lys Asp Glu Pro Arg Met Val
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Lys Phe Ser Trp Ile Phe Asp Arg Glu Ala Val Val
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<213> Oryza sativa

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His Ala Phe Val Tyr Thr Ala Phe Gln Glu Arg Ala Thr Ala Val Ala
35 40 45

His Gly Asn Thr Ala Arg Leu Val Gly Ala Arg Gly His Gly Asp Ala
 50 55 60
 Ala Leu Ala Arg Val Cys Gly Thr Val Ala Ala Asp Glu Lys Arg His
 65 70 75 80
 Glu Ala Ala Tyr Thr Arg Ile Val Ser Arg Leu Leu Glu Ala Asp Pro
 85 90 95
 Asp Ala Gly Val Arg Ala Val Ala Arg Met Leu Arg Arg Gly Val Ala
 100 105 110
 Met Pro Thr Ser Pro Ile Ser Asp Gly Arg Arg Asp Asp Leu Tyr Ala
 115 120 125
 Cys Val Val Ser Leu Ala Glu Gln Ala Gly Thr Tyr Thr Val Ser Asp
 130 135 140
 Tyr Cys Ser Ile Val Glu His Leu Val Arg Glu Trp Arg Val Glu Glu
 145 150 155 160
 Leu Ala Ala Gly Leu Ser Gly Glu Gly Arg Ala Arg Asp Tyr Val
 165 170 175
 Cys Glu Leu Pro Gln Lys Ile Arg Arg Met Lys Glu Lys Ala His Glu
 180 185 190
 Arg Ala Val Lys Ala Gln Lys Lys Pro Ile Ser Ile Pro Ile Asn Trp
 195 200 205
 Ile Phe Asp Arg His Val Ser Val Met Leu Pro
 210 215

<210> 15
 <211> 1318
 <212> DNA
 <213> *Oryza sativa*

<400> 15
 gcacgagaac tagctactgt agttgactga cagtgatagt ggcagtcattg caggtcgtgg 60
 gaaccgtgcg tgtcagtggc tgcggcgcg tggtagcgcc ctgcgcgcg cagtgcgcg 120
 tgtccgcggc ggtgctgacg gccgcggaga cggcgacggc gacgcggcg cgcgtgacgc 180
 actcgatgcc gccggagaag gcggaggtgt tccggtcgct ggaaggggtg gcgaggtcgt 240
 cgctgctgcc gctgctcaag cccgtggagg agtgctggca gccgacggac ttcttgccgg 300
 actcgtcgtc ggagatgttc gagcaccagg tccacgagct ccgcgcgcgc gccgcggggc 360
 tccccgacga gtacttcgtc gtgctggtcg gggacatgat taccgaggag gcgctgccga 420
 cgtaccagac catgatcaac acgtcgcagc gcgtccgcga cgagaccggc gccagcgcct 480
 gccctggggc cgtctggacg cgcacctgga ccgcgcgagg gaaccgccac ggcgacatcc 540
 tcggcaagta catgtacctc tccggccgcg tcgacatgcg catggtcgag aagaccgtcc 600
 agtacctcat cggctccggc atggatccgg ggacggagaa caaccgtac ctgggggttcg 660
 tgtacaccag cttccaggag cgcgcgacgg ccgtgtcgca cgggaacacg gcgcgcctcg 720
 ccagggcgca cggggacgac gtcttgccgc gcacctgcgg caccatcgcc gccgacgaga 780
 agcggcacga gacggcgtag gggcgcatcg tggagcagct gctgcggctc gaccgggacg 840
 gcgccatgct cgccatcgcc gacatgatgc acaagcggat caccatgcc gccgcacctca 900
 tgcacgacgg ccgcgacatg aacctgttcg accacttcgc cgcggtggcg cagcgcctca 960
 acgtctacac cgcgcgcgac tacgccgaca tcgtcgagtt cctcgtcaag cgggtggaagc 1020
 tggagaccct ggagactggg ctctccggcg agggccggag ggcccgggc ttctgtgtcg 1080
 ggctcgcgaa gaggatgcgg cgggcccgcg agcgggctga ggacagggtc aagaaggatg 1140
 agcagaggaa ggtcaagttc agctggatct atgataggga agtgattgtc tagtttaact 1200

tgtcttgggtt gaattctgaa ttcccagtc tagatgatca tgccatttcg ttatcatctc 1260
 tgttcttgtg ttctctttgc aatgcagtaa attggtaata aaaaaaaaaa aaaaaaaa 1318

<210> 16
 <211> 381
 <212> PRT
 <213> Oryza sativa

<400> 16
 Met Gln Val Val Gly Thr Val Arg Val Ser Gly Cys Gly Ala Val Val
 1 5 10 15
 Ala Pro Ser Arg Arg Gln Cys Arg Val Ser Ala Ala Val Leu Thr Ala
 20 25 30
 Ala Glu Thr Ala Thr Ala Thr Arg Arg Arg Val Thr His Ser Met Pro
 35 40 45
 Pro Glu Lys Ala Glu Val Phe Arg Ser Leu Glu Gly Trp Ala Arg Ser
 50 55 60
 Ser Leu Leu Pro Leu Leu Lys Pro Val Glu Glu Cys Trp Gln Pro Thr
 65 70 75 80
 Asp Phe Leu Pro Asp Ser Ser Ser Glu Met Phe Glu His Gln Val His
 85 90 95
 Glu Leu Arg Ala Arg Ala Ala Gly Leu Pro Asp Glu Tyr Phe Val Val
 100 105 110
 Leu Val Gly Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Gln Thr
 115 120 125
 Met Ile Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala Ser Ala
 130 135 140
 Cys Pro Trp Ala Val Trp Thr Arg Thr Trp Thr Ala Glu Glu Asn Arg
 145 150 155 160
 His Gly Asp Ile Leu Gly Lys Tyr Met Tyr Leu Ser Gly Arg Val Asp
 165 170 175
 Met Arg Met Val Glu Lys Thr Val Gln Tyr Leu Ile Gly Ser Gly Met
 180 185 190
 Asp Pro Gly Thr Glu Asn Asn Pro Tyr Leu Gly Phe Val Tyr Thr Ser
 195 200 205
 Phe Gln Glu Arg Ala Thr Ala Val Ser His Gly Asn Thr Ala Arg Leu
 210 215 220
 Ala Arg Ala His Gly Asp Asp Val Leu Ala Arg Thr Cys Gly Thr Ile
 225 230 235 240
 Ala Ala Asp Glu Lys Arg His Glu Thr Ala Tyr Gly Arg Ile Val Glu
 245 250 255
 Gln Leu Leu Arg Leu Asp Pro Asp Gly Ala Met Leu Ala Ile Ala Asp
 260 265 270

Met Met His Lys Arg Ile Thr Met Pro Ala His Leu Met His Asp Gly
275 280 285

Arg Asp Met Asn Leu Phe Asp His Phe Ala Ala Val Ala Gln Arg Leu
290 295 300

Asn Val Tyr Thr Ala Arg Asp Tyr Ala Asp Ile Val Glu Phe Leu Val
305 310 315 320

Lys Arg Trp Lys Leu Glu Thr Leu Glu Thr Gly Leu Ser Gly Glu Gly
325 330 335

Arg Arg Ala Arg Asp Phe Val Cys Gly Leu Ala Lys Arg Met Arg Arg
340 345 350

Ala Ala Glu Arg Ala Glu Asp Arg Ala Lys Lys Asp Glu Gln Arg Lys
355 360 365

Val Lys Phe Ser Trp Ile Tyr Asp Arg Glu Val Ile Val
370 375 380

<210> 17
<211> 384
<212> PRT
<213> Lupinus luteus

<400> 17

Met Gln Ile Gln Thr Cys Tyr Ser Ile Arg Ile Gln Ile Leu Pro Leu
1 5 10 15

Pro Trp Ala Arg Arg Thr Gly Arg His Lys Met Leu Pro Pro Ile Ala
20 25 30

Ala Ile Ser Ala Thr Pro Pro Ser Leu Lys Ser Pro Lys Thr His Ser
35 40 45

Met Pro Pro Glu Lys Ile Glu Ile Phe Lys Ser Leu Glu Ser Trp Ala
50 55 60

Ser Gln Ser Val Leu Pro Leu Leu Lys Pro Val Glu Gln Cys Trp Gln
65 70 75 80

Pro Gln Glu Phe Val Pro Asp Ser Ser Leu Pro Phe Gly Asp Phe Thr
85 90 95

Asp Gln Val Lys Ala Leu Arg Asp Arg Thr Ala Glu Leu Pro Glu Glu
100 105 110

Tyr Phe Val Val Leu Val Gly Asp Met Ile Thr Glu Asp Ala Leu Pro
115 120 125

Thr Tyr Gln Ser Met Ile Asn Asn Leu Asp Gly Val Arg Asp Glu Thr
130 135 140

Gly Ser Ser Pro Ser Pro Trp Ala Leu Trp Thr Arg Ala Trp Thr Ala
145 150 155 160

Glu Glu Lys Arg His Gly Asp Leu Leu Arg Thr Tyr Leu Tyr Leu Ser
 165 170 175
 Gly Arg Val Asp Met Lys Lys Ile Glu Lys Thr Val Gln Tyr Leu Ile
 180 185 190
 Gly Ser Gly Met Asp Pro Gly Thr Glu Asn Asn Pro Tyr Leu Gly Phe
 195 200 205
 Val Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Val Ser His Gly Asn
 210 215 220
 Thr Ala Arg Leu Ala Lys Glu Gly Gly Asp Pro Val Leu Ala Arg Ile
 225 230 235 240
 Cys Gly Thr Ile Ala Ala Asp Glu Lys Arg His Glu Asn Ala Tyr Ser
 245 250 255
 Arg Ile Val Glu Lys Leu Leu Glu Leu Asp Pro Thr Gly Ala Met Val
 260 265 270
 Ala Ile Gly Asp Met Met Gln Lys Lys Ile Thr Met Pro Ala His Leu
 275 280 285
 Met Tyr Asp Gly Glu Asp Pro Lys Leu Phe Asp His Phe Ser Ala Val
 290 295 300
 Ala Gln Arg Met Gly Val Tyr Thr Ala Asn Asp Tyr Ala Asp Ile Leu
 305 310 315 320
 Glu Phe Leu Ile Gly Arg Trp Arg Leu Glu Lys Val Gln Asp Leu Lys
 325 330 335
 Asp Glu Gly Lys Lys Ala Gln Asp Phe Val Cys Gly Leu Ala Pro Arg
 340 345 350
 Ile Arg Arg Leu Gln Glu Arg Ala Asp Glu Arg Ala Arg Lys Met Lys
 355 360 365
 Pro His Ala Val Lys Phe Ser Trp Ile Phe Asn Lys Glu Ile Ile Leu
 370 375 380

<210> 18

<211> 396

<212> PRT

<213> Cucumis sativus

<400> 18

Met Ala Leu Lys Phe His Pro Leu Thr Ser Gln Ser Pro Lys Leu Pro
 1 5 10 15

Ser Phe Arg Met Pro Gln Leu Ala Ser Leu Arg Ser Pro Lys Phe Val
 20 25 30

Met Ala Ser Thr Leu Arg Ser Thr Ser Arg Glu Val Glu Thr Leu Lys
 35 40 45

Lys Pro Phe Met Pro Pro Arg Glu Val His Leu Gln Val Thr His Ser
 50 55 60

Met	Pro	Pro	Gln	Lys	Met	Glu	Ile	Phe	Lys	Ser	Leu	Glu	Asp	Trp	Ala	
65					70					75					80	
Glu	Glu	Asn	Leu	Leu	Val	His	Leu	Lys	Pro	Val	Glu	Arg	Cys	Trp	Gln	
			85						90					95		
Pro	Gln	Asp	Phe	Leu	Pro	Asp	Ser	Ala	Phe	Glu	Gly	Phe	His	Glu	Gln	
			100					105					110			
Val	Arg	Glu	Leu	Arg	Glu	Arg	Ala	Lys	Glu	Leu	Pro	Asp	Glu	Tyr	Phe	
		115					120					125				
Val	Val	Leu	Val	Gly	Asp	Met	Ile	Thr	Glu	Glu	Ala	Leu	Pro	Thr	Tyr	
	130					135					140					
Gln	Thr	Met	Leu	Asn	Thr	Leu	Asp	Gly	Val	Arg	Asp	Glu	Thr	Gly	Ala	
145					150					155					160	
Ser	Pro	Thr	Pro	Trp	Ala	Ile	Trp	Thr	Arg	Ala	Trp	Thr	Ala	Glu	Glu	
				165					170					175		
Asn	Arg	His	Gly	Asp	Leu	Leu	Asn	Lys	Tyr	Leu	Tyr	Leu	Ser	Gly	Arg	
			180					185					190			
Val	Asp	Met	Arg	Gln	Val	Glu	Lys	Thr	Ile	Gln	Tyr	Leu	Ile	Gly	Ser	
		195					200					205				
Gly	Met	Asp	Pro	Arg	Thr	Glu	Asn	Asn	Pro	Tyr	Leu	Gly	Phe	Ile	Tyr	
	210					215					220					
Thr	Ser	Phe	Gln	Glu	Arg	Ala	Thr	Phe	Ile	Ser	His	Gly	Asn	Thr	Ala	
225					230					235					240	
Arg	Leu	Ala	Lys	Glu	His	Gly	Asp	Ile	Lys	Leu	Ala	Gln	Ile	Cys	Gly	
				245					250					255		
Thr	Ile	Thr	Ala	Asp	Glu	Lys	Arg	His	Glu	Thr	Ala	Tyr	Thr	Lys	Ile	
			260					265					270			
Val	Glu	Lys	Leu	Phe	Glu	Ile	Asp	Pro	Glu	Gly	Thr	Val	Ile	Ala	Phe	
		275					280					285				
Glu	Glu	Met	Met	Arg	Lys	Lys	Val	Ser	Met	Pro	Ala	His	Leu	Met	Tyr	
	290					295					300					
Asp	Gly	Arg	Asp	Asp	Asn	Leu	Phe	His	His	Phe	Ser	Ala	Val	Ala	Gln	
305					310					315					320	
Arg	Leu	Gly	Val	Tyr	Thr	Ala	Lys	Asp	Tyr	Ala	Asp	Ile	Leu	Glu	Phe	
				325					330					335		
Leu	Val	Gly	Arg	Trp	Lys	Val	Glu	Ser	Leu	Thr	Gly	Leu	Ser	Gly	Glu	
			340					345					350			
Gly	Gln	Lys	Ala	Gln	Asp	Tyr	Val	Cys	Ala	Leu	Pro	Ala	Arg	Ile	Arg	
		355					360					365				
Lys	Leu	Glu	Glu	Arg	Ala	Gln	Gly	Arg	Ala	Lys	Glu	Gly	Pro	Thr	Ile	
	370					375					380					

Pro Phe Ser Trp Ile Phe Asp Arg Gln Val Lys Leu
 385 390 395

<210> 19

<211> 374

<212> PRT

<213> Arabidopsis thaliana

<400> 19

Met Pro Ser Pro Ser Thr Phe Leu Ala Ser Arg Pro Arg Gly Pro Ala
 1 5 10 15

Lys Ile Ser Ala Val Ala Ala Pro Val Arg Pro Ala Leu Lys His Gln
 20 25 30

Asn Lys Ile His Thr Met Pro Pro Glu Lys Met Glu Ile Phe Lys Ser
 35 40 45

Leu Asp Gly Trp Ala Lys Asp Gln Ile Leu Pro Leu Leu Lys Pro Val
 50 55 60

Asp Gln Cys Trp Gln Pro Ala Ser Phe Leu Pro Asp Pro Ala Leu Pro
 65 70 75 80

Phe Ser Glu Phe Thr Asp Gln Val Arg Glu Leu Arg Glu Arg Thr Ala
 85 90 95

Ser Leu Pro Asp Glu Tyr Phe Val Val Leu Val Gly Asp Met Ile Thr
 100 105 110

Glu Asp Ala Leu Pro Thr Tyr Gln Thr Met Ile Asn Thr Leu Asp Gly
 115 120 125

Val Arg Asp Glu Thr Gly Ala Ser Glu Ser Ala Trp Ala Ser Trp Thr
 130 135 140

Arg Ala Trp Thr Ala Glu Glu Asn Arg His Gly Asp Leu Leu Arg Thr
 145 150 155 160

Tyr Leu Tyr Leu Ser Gly Arg Val Asp Met Leu Met Val Glu Arg Thr
 165 170 175

Val Gln His Leu Ile Gly Ser Gly Met Asp Pro Gly Thr Glu Asn Asn
 180 185 190

Pro Tyr Leu Gly Phe Val Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe
 195 200 205

Val Ser His Gly Asn Thr Ala Arg Leu Ala Lys Ser Ala Gly Asp Pro
 210 215 220

Val Leu Ala Arg Ile Cys Gly Thr Ile Ala Ala Asp Glu Lys Arg His
 225 230 235 240

Glu Asn Ala Tyr Val Arg Ile Val Glu Lys Leu Leu Glu Ile Asp Pro
 245 250 255

Asn Gly Ala Val Ser Ala Val Ala Asp Met Met Arg Lys Lys Ile Thr
 260 265 270
 Met Pro Ala His Leu Met Thr Asp Gly Arg Asp Pro Met Leu Phe Glu
 275 280 285
 His Phe Ser Ala Val Ala Gln Arg Leu Glu Val Tyr Thr Ala Asp Asp
 290 295 300
 Tyr Ala Asp Ile Leu Glu Phe Leu Val Gly Arg Trp Arg Leu Glu Lys
 305 310 315 320
 Leu Glu Gly Leu Thr Gly Glu Gly Gln Arg Ala Gln Glu Phe Val Cys
 325 330 335
 Gly Leu Ala Gln Arg Ile Arg Arg Leu Gln Glu Arg Ala Asp Glu Arg
 340 345 350
 Ala Lys Lys Leu Lys Lys Thr His Glu Val Cys Phe Ser Trp Ile Phe
 355 360 365
 Asp Lys Gln Ile Ser Val
 370

<210> 20
 <211> 398
 <212> PRT
 <213> Simmondsia chinensis

<400> 20
 Met Ala Leu Lys Leu His His Thr Ala Phe Asn Pro Ser Met Ala Val
 1 5 10 15
 Thr Ser Ser Gly Leu Pro Arg Ser Tyr His Leu Arg Ser His Arg Val
 20 25 30
 Phe Met Ala Ser Ser Thr Ile Gly Ile Thr Ser Lys Glu Ile Pro Asn
 35 40 45
 Ala Lys Lys Pro His Met Pro Pro Arg Glu Ala His Val Gln Lys Thr
 50 55 60
 His Ser Met Pro Pro Gln Lys Ile Glu Ile Phe Lys Ser Leu Glu Gly
 65 70 75 80
 Trp Ala Glu Glu Asn Val Leu Val His Leu Lys Pro Val Glu Lys Cys
 85 90 95
 Trp Gln Pro Gln Asp Phe Leu Pro Asp Pro Ala Ser Glu Gly Phe Met
 100 105 110
 Asp Gln Val Lys Glu Leu Arg Glu Arg Thr Lys Glu Ile Pro Asp Glu
 115 120 125
 Tyr Leu Val Val Leu Val Gly Asp Met Ile Thr Glu Glu Ala Leu Pro
 130 135 140
 Thr Tyr Gln Thr Met Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr
 145 150 155 160

Gly Ala Ser Leu Thr Ser Trp Ala Ile Trp Thr Arg Ala Trp Thr Ala
 165 170 175
 Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Leu Tyr Leu Thr
 180 185 190
 Gly Arg Val Asp Met Lys Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile
 195 200 205
 Gly Ser Gly Met Asp Pro Arg Ser Glu Asn Asn Pro Tyr Leu Gly Phe
 210 215 220
 Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn
 225 230 235 240
 Thr Ala Arg Leu Ala Lys Asp His Gly Asp Phe Gln Leu Ala Gln Val
 245 250 255
 Cys Gly Ile Ile Ala Ala Asp Glu Lys Arg His Glu Thr Ala Tyr Thr
 260 265 270
 Lys Ile Val Glu Lys Leu Phe Glu Ile Asp Pro Asp Gly Ala Val Leu
 275 280 285
 Ala Leu Ala Asp Met Met Arg Lys Lys Val Ser Met Pro Ala His Leu
 290 295 300
 Met Tyr Asp Gly Lys Asp Asp Asn Leu Phe Glu Asn Tyr Ser Ala Val
 305 310 315 320
 Ala Gln Gln Ile Gly Val Tyr Thr Ala Lys Asp Tyr Ala Asp Ile Leu
 325 330 335
 Glu His Leu Val Asn Arg Trp Lys Val Glu Asn Leu Met Gly Leu Ser
 340 345 350
 Gly Glu Gly His Lys Ala Gln Asp Phe Val Cys Gly Leu Ala Pro Arg
 355 360 365
 Ile Arg Lys Leu Gly Glu Arg Ala Gln Ser Leu Ser Lys Pro Val Ser
 370 375 380
 Leu Val Pro Phe Ser Trp Ile Phe Asn Lys Glu Leu Lys Val
 385 390 395

<210> 21

<211> 411

<212> PRT

<213> Arabidopsis thaliana

<400> 21

Met Ala Leu Leu Leu Asn Ser Thr Ile Thr Val Ala Met Lys Gln Asn
 1 5 10 15

Pro Leu Val Ala Val Ser Phe Pro Arg Thr Thr Cys Leu Gly Ser Ser
 20 25 30

Phe	Ser	Pro	Pro	Arg	Leu	Leu	Arg	Val	Ser	Cys	Val	Ala	Thr	Asn	Pro		
		35					40					45					
Ser	Lys	Thr	Ser	Glu	Glu	Thr	Asp	Lys	Lys	Lys	Phe	Arg	Pro	Ile	Lys		
	50					55					60						
Glu	Val	Pro	Asn	Gln	Val	Thr	His	Thr	Ile	Thr	Gln	Glu	Lys	Leu	Glu		
65					70					75					80		
Ile	Phe	Lys	Ser	Met	Glu	Asn	Trp	Ala	Gln	Glu	Asn	Leu	Leu	Ser	Tyr		
				85					90					95			
Leu	Lys	Pro	Val	Glu	Ala	Ser	Trp	Gln	Pro	Gln	Asp	Phe	Leu	Pro	Glu		
			100					105					110				
Thr	Asn	Asp	Glu	Asp	Arg	Phe	Tyr	Glu	Gln	Val	Lys	Glu	Leu	Arg	Asp		
		115					120					125					
Arg	Thr	Lys	Glu	Ile	Pro	Asp	Asp	Tyr	Phe	Val	Val	Leu	Val	Gly	Asp		
	130					135					140						
Met	Ile	Thr	Glu	Glu	Ala	Leu	Pro	Thr	Tyr	Gln	Thr	Thr	Leu	Asn	Thr		
145					150					155					160		
Leu	Asp	Gly	Val	Lys	Asp	Glu	Thr	Gly	Gly	Ser	Leu	Thr	Pro	Trp	Ala		
				165					170					175			
Val	Trp	Val	Arg	Ala	Trp	Thr	Ala	Glu	Glu	Asn	Arg	His	Gly	Asp	Leu		
			180					185					190				
Leu	Asn	Lys	Tyr	Leu	Tyr	Leu	Ser	Gly	Arg	Val	Asp	Met	Arg	His	Val		
		195					200					205					
Glu	Lys	Thr	Ile	Gln	Tyr	Leu	Ile	Gly	Ser	Gly	Met	Asp	Ser	Lys	Phe		
	210					215					220						
Glu	Asn	Asn	Pro	Tyr	Asn	Gly	Phe	Ile	Tyr	Thr	Ser	Phe	Gln	Glu	Arg		
225					230					235					240		
Ala	Thr	Phe	Ile	Ser	His	Gly	Asn	Thr	Ala	Lys	Leu	Ala	Thr	Thr	Tyr		
				245					250					255			
Gly	Asp	Thr	Thr	Leu	Ala	Lys	Ile	Cys	Gly	Thr	Ile	Ala	Ala	Asp	Glu		
			260					265					270				
Lys	Arg	His	Glu	Thr	Ala	Tyr	Thr	Arg	Ile	Val	Glu	Lys	Leu	Phe	Glu		
		275					280					285					
Ile	Asp	Pro	Asp	Gly	Thr	Val	Gln	Ala	Leu	Ala	Ser	Met	Met	Arg	Lys		
	290					295					300						
Arg	Ile	Thr	Met	Pro	Ala	His	Leu	Met	His	Asp	Gly	Arg	Asp	Asp	Asp		
305					310					315					320		
Leu	Phe	Asp	His	Tyr	Ala	Ala	Val	Ala	Gln	Arg	Ile	Gly	Val	Tyr	Thr		
				325					330					335			
Ala	Thr	Asp	Tyr	Ala	Gly	Ile	Leu	Glu	Phe	Leu	Leu	Arg	Arg	Trp	Glu		
			340					345						350			

Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn Thr Ala Arg
 225 230 235 240
 Leu Ala Lys Asp His Gly Asp Met Lys Leu Ala Gln Ile Cys Gly Ile
 245 250 255
 Ile Ala Ala Asp Glu Lys Arg His Glu Thr Ala Tyr Thr Lys Ile Val
 260 265 270
 Glu Lys Leu Phe Glu Ile Asp Pro Asp Gly Thr Val Leu Ala Leu Ala
 275 280 285
 Asp Met Met Arg Lys Lys Ile Ser Met Pro Ala His Leu Met Tyr Asp
 290 295 300
 Gly Glu Asp Asp Asn Leu Phe Asp Asn Tyr Ser Ser Val Ala Gln Arg
 305 310 315 320
 Ile Gly Val Tyr Thr Ala Lys Asp Tyr Ala Asp Ile Leu Glu Phe Leu
 325 330 335
 Val Gly Arg Trp Lys Val Asp Ala Phe Thr Gly Leu Ser Gly Glu Gly
 340 345 350
 Asn Lys Ala Gln Asp Phe Val Cys Gly Leu Pro Ala Arg Ile Arg Lys
 355 360 365
 Leu Glu Glu Arg Ala Ala Gly Arg Ala Lys Gln Thr Ser Lys Ser Val
 370 375 380
 Pro Phe Ser Trp Ile Phe Ser Arg Glu Leu Val Leu
 385 390 395

<210> 23

<211> 391

<212> PRT

<213> Glycine max

<400> 23

Met ala Leu Arg Leu Asn Pro Ile Pro Thr Gln Thr Phe Ser Leu Pro
 1 5 10 15

Gln Met Pro Ser Leu Arg Ser Pro Arg Phe Arg Met ala Ser Thr Leu
 20 25 30

Arg Ser Gly Ser Lys Glu Val Glu Asn Ile Lys Lys Pro Phe Thr Pro
 35 40 45

Pro Arg Glu Val His Val Gln Val Thr His Ser Met Pro Pro Gln Lys
 50 55 60

Ile Glu Ile Phe Lys Ser Leu Glu Asp Trp Ala Asp Gln Asn Ile Leu
 65 70 75 80

Thr His Leu Lys Pro Val Glu Lys Cys Trp Gln Pro Gln Asp Phe Leu
 85 90 95

Pro Asp Pro Ser Ser Asp Gly Phe Glu Glu Gln Val Lys Glu Leu Arg
 100 105 110
 Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe Val Val Leu Val Gly
 115 120 125
 Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Gln Thr Met Leu Asn
 130 135 140
 Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala Ser Leu Thr Ser Trp
 145 150 155 160
 Ala Ile Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn Arg His Gly Asp
 165 170 175
 Leu Leu Asn Lys Tyr Leu Tyr Leu Ser Gly Arg Val Asp Met Lys Gln
 180 185 190
 Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly Met Asp Pro Arg
 195 200 205
 Thr Glu Asn Ser Pro Tyr Leu Gly Phe Ile Tyr Thr Ser Phe Gln Glu
 210 215 220
 Arg Ala Thr Phe Ile Ser His Gly Asn Thr Ala Arg Leu Ala Lys Glu
 225 230 235 240
 His Gly Asp Ile Lys Leu Ala Gln Ile Cys Gly Met Ile Ala Ser Asp
 245 250 255
 Glu Lys Arg His Glu Thr Ala Tyr Thr Lys Ile Val Glu Lys Leu Phe
 260 265 270
 Glu Val Asp Pro Asp Gly Thr Val Met ala Phe Ala Asp Met Met Arg
 275 280 285
 Lys Lys Ile Ala Met Pro Ala His Leu Met Tyr Asp Gly Arg Asp Asp
 290 295 300
 Asn Leu Phe Asp Asn Tyr Ser Ala Val Ala Gln Arg Ile Gly Val Tyr
 305 310 315 320
 Thr Ala Lys Asp Tyr Ala Asp Ile Leu Glu Phe Leu Val Gly Arg Trp
 325 330 335
 Lys Val Glu Gln Leu Thr Gly Leu Ser Gly Glu Gly Arg Lys Ala Gln
 340 345 350
 Glu Tyr Val Cys Gly Leu Pro Pro Arg Ile Arg Arg Leu Glu Glu Arg
 355 360 365
 Ala Gln Ala Arg Gly Lys Glu Ser Ser Thr Leu Lys Phe Ser Trp Ile
 370 375 380
 His Asp Arg Glu Val Leu Leu
 385 390

<210> 24

<211> 80

<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: ELVISLIVES complementary region of pKS106 and pKS124

<400> 24

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cggccggagc tggatcatctc gctcatcgtc gagtcggcgg ccgcccagctc gacgatgagc 60
gagatgacca gctccggccg                                     80
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<210> 25

<211> 154

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: ELVISLIVES complementary region of pKS133

<400> 25

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cggccggagc tggatcatctc gctcatcgtc gagtcggcgg ccggagctgg tcatctcgct 60
catcgtcgag tcggcgcccg ccgactcgac gatgagcgag atgaccagct ccggccgccc 120
actcgacgat gagcgagatg accagctccg gccg                                     154
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<210> 26

<211> 6611

<212> DNA

<213> Plasmid pBS68

<220>

<221> Unsure

<222> (4436)..(4436)

<223> n = A, C, G, or T

<400> 26

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tcgtggagaa gcttctggaa gtggacccca ccggggcaat ggtggccata gggaacatga 120
tggagaagaa gatcacgatg ccggcgcacc ttatgtacga tgggatgac cccaggetat 180
tcgagacta ctccgctgtg gcgcagcgca taggcgtgta caccgccaac gactacgcag 240
acatcttgga tttctcgctg acggtgaaga ttggagaagc ttgaaggatt gatgcctgag 300
gggaagcggg ccccaggatt tccgtgtgtg ggttgcccc gaggattagg aggttccaag 360
aacgcgctga tgagcgagcg cgtaagatga agaagcatca tgccgttaag ttcagttgga 420
ttttcaataa agaattgctt ttgtgagcgg ccgcccagctc gacgatgagc gagatgacca 480
gtcccgcccg ccgactcgac gatgagcgag atgaccagct ccggccgcca cacaagtgtg 540
agagtactaa ataaatgctt tggttgtacg aaatcattac actaaataaa ataatcaaag 600
cttatatatg ccttccgcta aggcggaatg caaagaaatt ggttctttct cgttatcttt 660
tgccactttt actagtacgt attaattact acttaatcat ctttgtttac ggctcattat 720
atccgtcgac ggcgcgccc atcatccgga tatagttcct cctttcagca aaaaaccocct 780
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